

RAW SEQUENCE LISTING

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Application Serial Number:

091913,772A

Source:

IFW/6

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IFW16

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/913,772A

DATE: 03/04/2005
TIME: 08:30:18

Input Set : A:\PTO.SR.txt
Output Set: N:\CRF4\03042005\I913772A.raw

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3 <110> APPLICANT: RENNO Toufic
4      BONNEFOY Jean-Yves
6 <120> TITLE OF INVENTION: USE OF AN ENTEROBACTERIUM OmpA PROTEIN ASSOCIATED WITH AN
7      ANTIGEN FOR GENERATING AN ANTIVIRAL, ANTIPARASITIC OR
8      ANTITUMORAL CYTOTOXIC RESPONSE
10 <130> FILE REFERENCE: D 17921
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/913,772A
C--> 13 <141> CURRENT FILING DATE: 2001-09-24
15 <150> PRIOR APPLICATION NUMBER: FR 99 01917
16 <151> PRIOR FILING DATE: 1999-02-17
18 <160> NUMBER OF SEQ ID NOS: 6
20 <170> SOFTWARE: PatentIn Ver. 2.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 1035
24 <212> TYPE: DNA
25 <213> ORGANISM: Klebsiella pneumoniae
27 <220> FEATURE:
28 <221> NAME/KEY: exon
29 <222> LOCATION: (1)..(1032)
31 <220> FEATURE:
32 <221> NAME/KEY: terminator
33 <222> LOCATION: (1033)..(1035)
35 <220> FEATURE:
36 <221> NAME/KEY: CDS
37 <222> LOCATION: (1)..(1035)
39 <400> SEQUENCE: 1
40 atg aaa gca att ttc gta ctg aat gcg gct ccg aaa gat aac acc tgg      48
41 Met Lys Ala Ile Phe Val Leu Asn Ala Ala Pro Lys Asp Asn Thr Trp
42      1           5           10          15
44 tat gca ggt ggt aaa ctg ggt tgg tcc cag tat cac gac acc ggt ttc      96
45 Tyr Ala Gly Gly Lys Leu Gly Trp Ser Gln Tyr His Asp Thr Gly Phe
46      20          25          30
48 tac ggt aac ggt ttc cag aac aac ggt ccg acc cgt aac gat cag      144
49 Tyr Gly Asn Gly Phe Gln Asn Asn Gly Pro Thr Arg Asn Asp Gln
50      35          40          45
52 ctt ggt ggt gcg ttc ggt ggt tac cag gtt aac ccg tac ctc ggt      192
53 Leu Gly Ala Gly Ala Phe Gly Gly Tyr Gln Val Asn Pro Tyr Leu Gly
54      50          55          60
56 ttc gaa atg ggt tat gac tgg ctg ggc cgt atg gca tat aaa ggc agc      240
57 Phe Glu Met Gly Tyr Asp Trp Leu Gly Arg Met Ala Tyr Lys Gly Ser
58      65          70          75          80
60 gtt gac aac ggt gct ttc aaa gct cag ggc gtt cag ctg acc gct aaa      288
61 Val Asp Asn Gly Ala Phe Lys Ala Gln Gly Val Gln Leu Thr Ala Lys

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62	85	90	95	
64	ctg ggt tac ccg atc act gac gat	ctg gac atc tac acc cgt	ctg ggc	336
65	Leu Gly Tyr Pro Ile Thr Asp Asp	Leu Asp Ile Tyr Thr Arg	Leu Gly	
66	100	105	110	
68	ggc atg gtt tgg cgc gct gac tcc aaa	ggc aac tac gct tct acc ggc		384
69	Gly Met Val Trp Arg Ala Asp Ser	Lys Gly Asn Tyr Ala Ser Thr	Gly	
70	115	120	125	
72	gtt tcc cgt agc gaa cac gac act	ggc gtt tcc cca gta ttt gct ggc		432
73	Val Ser Arg Ser Glu His Asp Thr	Gly Val Ser Pro Val Phe Ala	Gly	
74	130	135	140	
76	ggc gta gag tgg gct gtt act cgt	gac atc gct acc cgt ctg gaa tac		480
77	Gly Val Glu Trp Ala Val Thr Arg	Asp Ile Ala Thr Arg Leu Glu	Tyr	
78	145	150	155	160
80	cag tgg gtt aac aac atc ggc gac	gcg act gtg ggt acc cgt cct		528
81	Gln Trp Val Asn Asn Ile Gly Asp	Ala Gly Thr Val Gly Thr Arg	Pro	
82	165	170	175	
84	gat aac ggc atg ctg agc ctg ggc	gtt tcc tac cgc ttc ggt cag gaa		576
85	Asp Asn Gly Met Leu Ser Leu Gly	Val Ser Tyr Arg Phe Gly Gln	Glu	
86	180	185	190	
88	gat gct gca ccg gtt gct ccg	gct ccg gct ccg gaa gtg		624
89	Asp Ala Ala Pro Val Val Ala Pro	Ala Pro Ala Pro Ala Pro Glu	Val	
90	195	200	205	
92	gct acc aag cac ttc acc ctg aag	tct gac gtt ctg ttc aac ttc aac		672
93	Ala Thr Lys His Phe Thr Leu Lys	Ser Asp Val Leu Phe Asn Phe	Asn	
94	210	215	220	
96	aaa gct acc ctg aaa ccg gaa	ggt cag cag gct ctg gat cag ctg tac		720
97	Lys Ala Thr Leu Lys Pro Glu Gly	Gln Gln Ala Leu Asp Gln Leu	Tyr	
98	225	230	235	240
100	act cag ctg agc aac atg gat	ccg aaa gac ggt tcc gct gtt gtt ctg		768
101	Thr Gln Leu Ser Asn Met Asp Pro	Lys Asp Gly Ser Ala Val Val	Leu	
102	245	250	255	
104	ggc tac acc gac cgc atc ggt	tcc gaa gct tac aac cag cag ctg tct		816
105	Gly Tyr Thr Asp Arg Ile Gly Ser	Ala Tyr Asn Gln Gln Leu Ser		
106	260	265	270	
108	gag aaa cgt gct cag tcc gtt	gac tac ctg gtt gct aaa ggc atc		864
109	Glu Lys Arg Ala Gln Ser Val Val	Asp Tyr Leu Val Ala Lys Gly Ile		
110	275	280	285	
112	ccg gct ggc aaa atc tcc gct	ccg ggc atg ggt gaa tcc aac ccg gtt		912
113	Pro Ala Gly Lys Ile Ser Ala Arg	Gly Met Gly Glu Ser Asn Pro Val		
114	290	295	300	
116	act ggc aac acc tgt gac aac	gtg aaa gct cgc gct gcc ctg atc gat		960
117	Thr Gly Asn Thr Cys Asp Asn Val	Lys Ala Arg Ala Ala Leu Ile Asp		
118	305	310	315	320
120	tgc ctg gct ccg gat cgt	ctg gta gag atc gaa gtt aaa ggc tac	aaa	1008
121	Cys Leu Ala Pro Asp Arg Arg Val	Glu Ile Glu Val Lys Gly Tyr Lys		
122	325	330	335	
124	gaa gtt gta act cag ccg gcg	ggt taa		1035
125	Glu Val Val Thr Gln Pro Ala	Gly		
126	340			

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129 <210> SEQ ID NO: 2
 130 <211> LENGTH: 344
 131 <212> TYPE: PRT
 132 <213> ORGANISM: Klebsiella pneumoniae
 134 <400> SEQUENCE: 2
 135 Met Lys Ala Ile Phe Val Leu Asn Ala Ala Pro Lys Asp Asn Thr Trp
 1 5 10 15
 138 Tyr Ala Gly Gly Lys Leu Gly Trp Ser Gln Tyr His Asp Thr Gly Phe
 20 25 30
 141 Tyr Gly Asn Gly Phe Gln Asn Asn Asn Gly Pro Thr Arg Asn Asp Gln
 35 40 45
 144 Leu Gly Ala Gly Ala Phe Gly Gly Tyr Gln Val Asn Pro Tyr Leu Gly
 50 55 60
 147 Phe Glu Met Gly Tyr Asp Trp Leu Gly Arg Met Ala Tyr Lys Gly Ser
 65 70 75 80
 150 Val Asp Asn Gly Ala Phe Lys Ala Gln Gly Val Gln Leu Thr Ala Lys
 85 90 95
 153 Leu Gly Tyr Pro Ile Thr Asp Asp Leu Asp Ile Tyr Thr Arg Leu Gly
 100 105 110
 156 Gly Met Val Trp Arg Ala Asp Ser Lys Gly Asn Tyr Ala Ser Thr Gly
 115 120 125
 159 Val Ser Arg Ser Glu His Asp Thr Gly Val Ser Pro Val Phe Ala Gly
 130 135 140
 162 Gly Val Glu Trp Ala Val Thr Arg Asp Ile Ala Thr Arg Leu Glu Tyr
 145 150 155 160
 165 Gln Trp Val Asn Asn Ile Gly Asp Ala Gly Thr Val Gly Thr Arg Pro
 165 170 175
 168 Asp Asn Gly Met Leu Ser Leu Gly Val Ser Tyr Arg Phe Gly Gln Glu
 180 185 190
 171 Asp Ala Ala Pro Val Val Ala Pro Ala Pro Ala Pro Ala Pro Glu Val
 195 200 205
 174 Ala Thr Lys His Phe Thr Leu Lys Ser Asp Val Leu Phe Asn Phe Asn
 210 215 220
 177 Lys Ala Thr Leu Lys Pro Glu Gly Gln Gln Ala Leu Asp Gln Leu Tyr
 225 230 235 240
 180 Thr Gln Leu Ser Asn Met Asp Pro Lys Asp Gly Ser Ala Val Val Leu
 245 250 255
 183 Gly Tyr Thr Asp Arg Ile Gly Ser Glu Ala Tyr Asn Gln Gln Leu Ser
 260 265 270
 186 Glu Lys Arg Ala Gln Ser Val Val Asp Tyr Leu Val Ala Lys Gly Ile
 275 280 285
 189 Pro Ala Gly Lys Ile Ser Ala Arg Gly Met Gly Glu Ser Asn Pro Val
 290 295 300
 192 Thr Gly Asn Thr Cys Asp Asn Val Lys Ala Arg Ala Ala Leu Ile Asp
 305 310 315 320
 195 Cys Leu Ala Pro Asp Arg Arg Val Glu Ile Glu Val Lys Gly Tyr Lys
 325 330 335
 198 Glu Val Val Thr Gln Pro Ala Gly
 199 340

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203 <210> SEQ ID NO: 3
204 <211> LENGTH: 10
205 <212> TYPE: PRT
206 <213> ORGANISM: Homo sapiens
208 <220> FEATURE:
209 <223> OTHER INFORMATION: Peptide derived from the Mart-1/MelanA antigen expressed by
210 melanoma cells.
212 <400> SEQUENCE: 3
213 Glu Leu Ala Gly Ile Gly Ile Leu Thr Val
214 1 5 10
217 <210> SEQ ID NO: 4
218 <211> LENGTH: 8
219 <212> TYPE: PRT
220 <213> ORGANISM: Homo sapiens
222 <220> FEATURE:
223 <223> OTHER INFORMATION: Derivative of tyrosinase-related protein 2 (TRP-2).
225 <400> SEQUENCE: 4
226 Val Tyr Asp Phe Phe Val Trp Leu
227 1 5
237 <210> SEQ ID NO: 5
238 <211> LENGTH: 9
239 <212> TYPE: PRT
240 <213> ORGANISM: Homo sapiens
242 <220> FEATURE:
243 <223> OTHER INFORMATION: Peptide derived from the Mart-1/MelanA antigen expressed by
244 melanoma cells.
246 <400> SEQUENCE: 5
247 Ala Ala Gly Ile Gly Ile Leu Thr Val
248 1 5
252 <210> SEQ ID NO: 6
253 <211> LENGTH: 10
254 <212> TYPE: PRT
255 <213> ORGANISM: Homo sapiens
257 <220> FEATURE:
258 <223> OTHER INFORMATION: Peptide derived from the Mart-1/MelanA antigen expressed by
259 melanoma cells.
261 <400> SEQUENCE: 6
262 Glu Ala Ala Gly Ile Gly Ile Leu Thr Val
263 1 5 10

VERIFICATION SUMMARY

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Input Set : A:\PTO.SR.txt

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L:12 M:270 C: Current Application Number differs, Replaced Current Application Number

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date